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100 kb

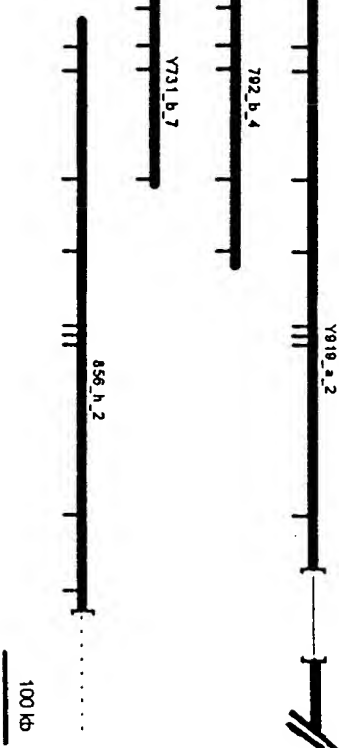
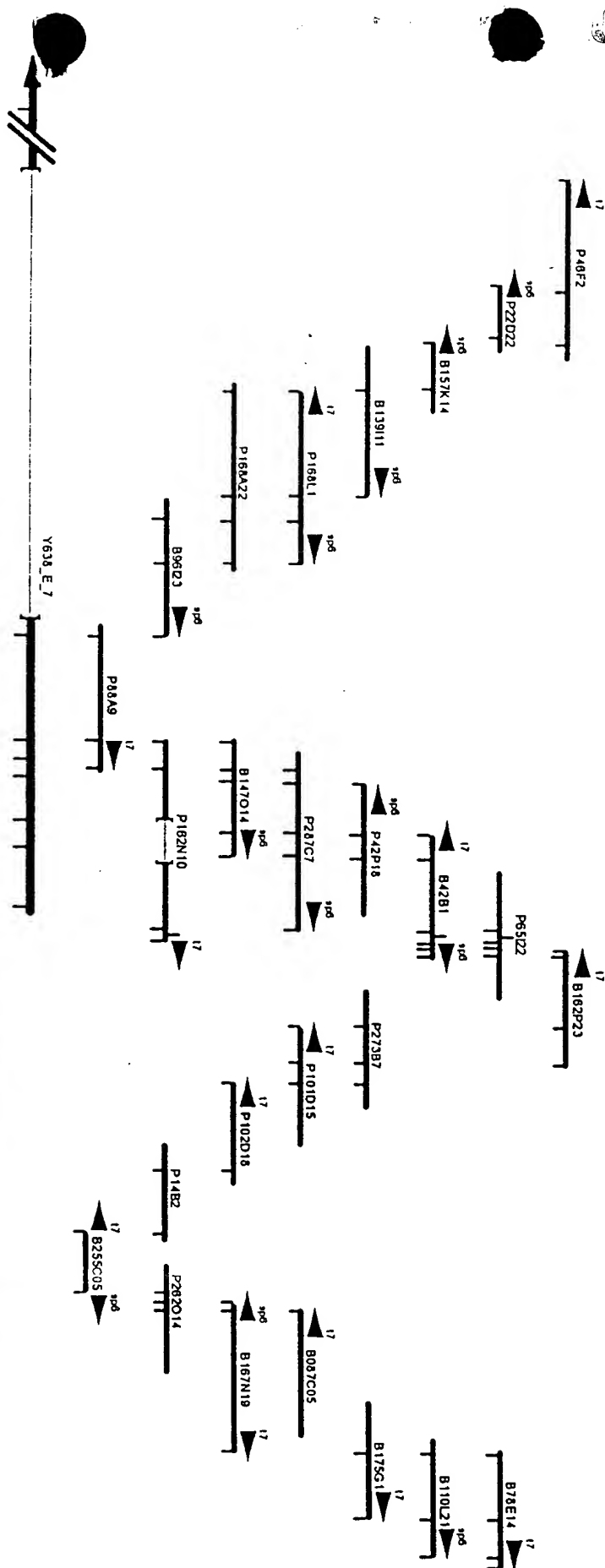


FIGURE 1

D12S1328
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 P22D22sp6
 B157K14sp6
 P168L1T7
 B139I11sp6
 D12S1332
 168L1sp6
 B96I23sp6
 B147O14CAG
 B88A9t7
 B42P18sp6
 B42B1t7
 B147O14sp6
 P287C7sp6
 B162N10t7
 P162P23t7
 B42B1sp6
 101D15t7
 ALDex6/12
 102D18t7
 D12S1333
 B255C05t7
 B255C05sp6
 B167N19sp6
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 B167N19t7
 B175g1t7
 B110L21sp6
 B78E14t7



[illegible]

FIGURE 2

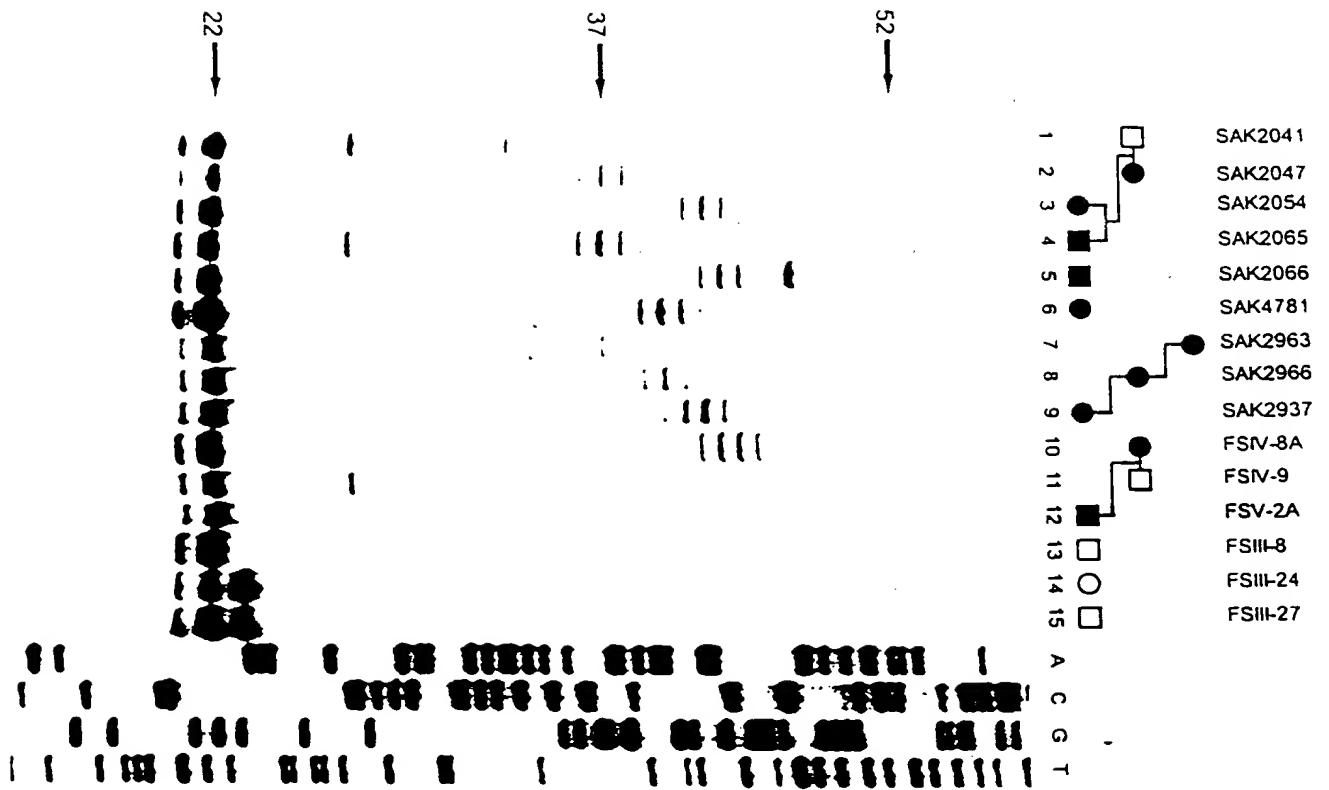


FIGURE 3

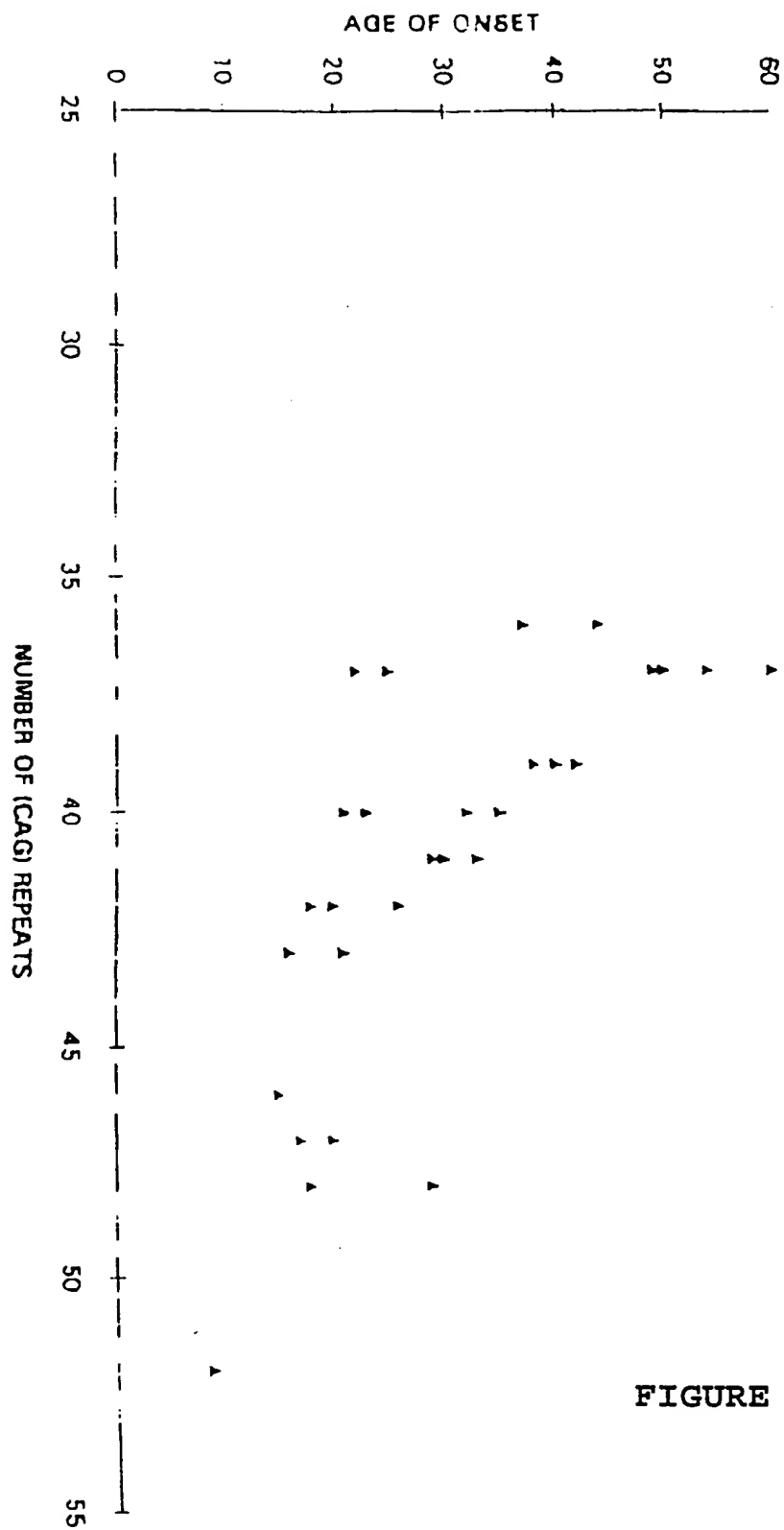


FIGURE 4

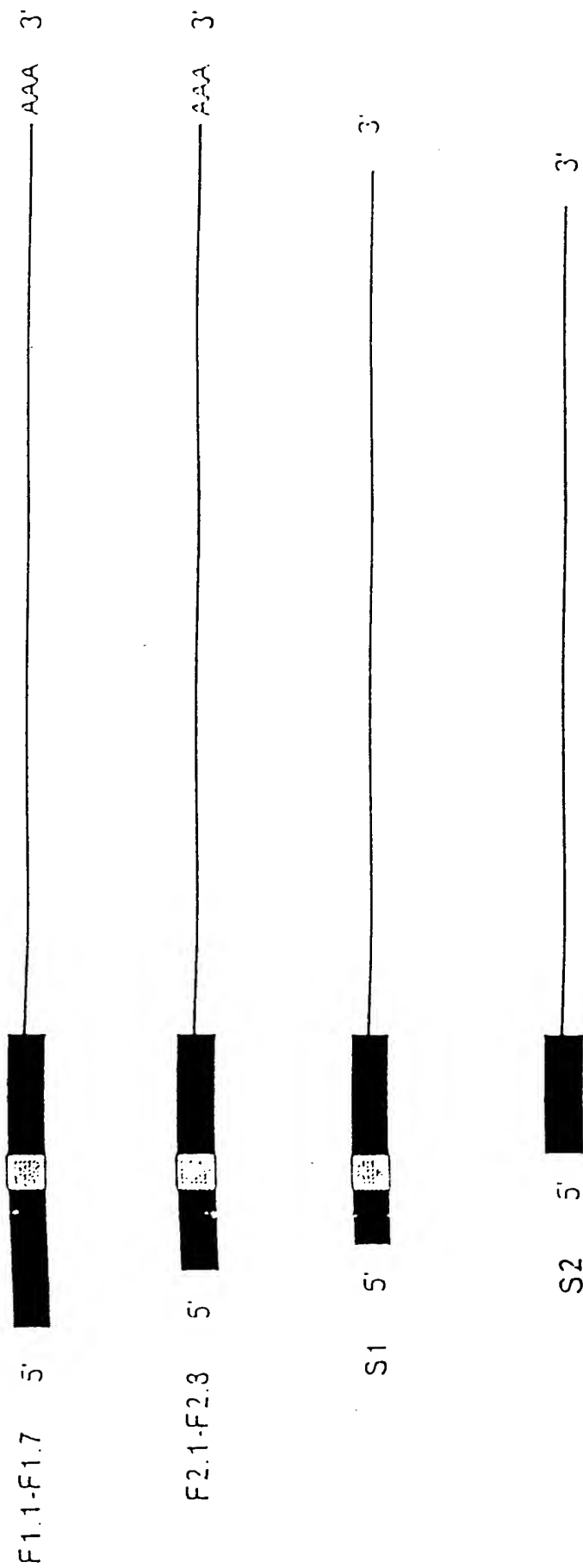


FIGURE 5

300 bp

1	ACCCCCGAGAAAGCAACCCAGCGCGCCGCCCGCTCCTCAGGTGTCCCTCCCGGCCCGGG	60
61	GCCACCTCAGCTTCTGCTTCCGTCTGACCCCTCCGACTTCCGGTAAAGAGTCCCTATCCG	120
121	CACCTCCGCTCCCAACCGGGGCGCTCGGCGCGCCCGCCCTCCGATGCGCTCAGCGGCCGCA	180
1	M R S A A A	6
181	GCTCCTCGGAGTCCCGGGTGGCCACCGAGTCTCGCCGCTTCGCCCGCAGCCAGGTGGCCC	240
7	A P R S P A V A T E S R R F A A A R W P	26
241	GGGTGGCGCTCGCTCCAGCGGCCCGCGCGGAGCGGGCGGGCGGGCGGTGGCGCGGCC	300
27	G W R S L Q R P A R R S G R G G G G A A	46
301	CCGGGACCGTATCCCTCCGCGCCCGCTCCCGCGCCCGCGCCCGCGCCCGCTCCCTCCCGG	360
47	P G P Y P S A A P P P G P G P P P S R	66
361	CAGAGCTCGCCTCCCTCCGCTCAGACTGTTTGGTAGCAACGGCAACGGCGCGCGCGCG	420
67	O S S P P S A S D C F G S N G N G G A	86
421	TTTCGGCCCGCTCCCGCGCGCTCCCTGGTCTCGCGCGCGCTCCCGCGCCCTTCGTCTC	480
87	F R P G S R R L L G L G G P P R P F V V	106
481	GTCCTTCTCCCGCTCGCCAGCCCGGGCGCCCGCTCCCGCGCGCCCAACCGCGCCCTCCCG	540
107	V L L P L A S P G A P P A A P T R A S P	126
541	CTCGGCGCCCGTCCGTCCCGCGCGCTTCCGGCGTCTCCTTGGCGCGCCCGGCTCCCGGC	600
127	L G A R A S P P R S G V S L A R P A P G	146
	SCA2-A	
601	TGTCCCGCGCCCGGCTCGGAGCGCGTGTATGGGCGCCCTCACCATGTGCTGAAGCCCCAG	660
147	C P R P A C E P V Y G P L T M S L K P Q	166
661	CAGCAGCAGCAGCAGCAGCAGCAACAGCAGCAGCAGCAACAGCAGCAGCAGCAGCAG	720
167	Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q	186
	SCA2-B	
721	CAGCCGCGCCCGCGGGCTGCCAATGTCCGCAAGCCCGGGCGGCAGCGGCCTTCTAGCGTCG	780
187	O P P P A A A N V R K P G G S G L I A S	206
781	CCCGCGCGCGCGCTTCGCGCTCCTCGTCTCCTCGTCTCCTCGTCTCCTCGGCCACGGCTCCC	840
207	P A A A P S P S S S S V S S S S A T A P	226
841	TCCTCGGTGGTGGCGCGGACCTCCGGCGGGCGGGAGGCCCGGCCCTGGGCAGAGGTGGAAC	900
227	S S V V A A T S G G G R P G L G R G R N	246
901	AGTAACAAGGACTGCTCAGTCTACGATTTCCTTTGATGGAATCTATGCAATATGAGG	960
247	S N K G L P Q S T I S F D G I Y A N M R	266
961	ATGGTTCATATACTTACATCAGTTGTTGGCTCCAAATGTGAAGTACAAGTGAAAAATGGA	1020
267	M V H I I T S V V G S K C E V Q V K N G	286
	SCA2-14B	
1021	GGTATATATGAAGGAGTTTAAAACTTACAGTCCGAAGTGTGATTTGGTACTTGTATGCC	1080
287	G I Y E G V F K T Y S P K C D L V L D A	306
1081	GCACATGAGAAAAAGTACAGAATCCAGTTCGGGGCCGAAACGTGAAGAAATAATGGAGAGT	1140
307	A H E K S T E S S S G P K R E E I M E S	326
1141	ATTTTGTTCAAATGTTCCAGACTTTGTTGTGGTACAGTTTAAAGATATGGACTCCAGTTAT	1200
327	I L F K C S D F V V V Q F K D M D S S Y	346
1201	GCAAAAAGAGATGCTTTTACTGACTCTGCTATCAGTGCTAAAGTGAATGGCGAACACAAA	1260
347	A K R D A F T D S A I S A K V H G E H K	366
1261	GAGAAGGAGCTGGAGGCTTGGGATGCAGGTGAACCTCAGCCCAATGAGGAACCTTGAGGCT	1320
367	E K D L E P W D A G E L T A N E E L E A	386
1321	TTGGAAATGACGTATCTAATGGATGGGATGCCAATGATATGTTTCGATATAATGAAGAA	1380
387	L E H D V S H G W D P H D H F R Y H E E	406
1381	AATTATGGTGTAGTGTCTACGTATGATAGCAGTTTATCTTCGTATACAGTCCCTTAGAA	1440
407	H Y G V V S T Y D S S L S S Y T V P L E	426
1441	AGAGATAACTCAGAAGAATTTTAAAAACGGGAAGCAAGGGCAAAACAGTTAGCAGAAGAA	1500
427	R D H S E E F L K R E A R A H Q L A E E	446

FIGURE 6A

1501	ATTGAGTCAAGTGCCCAAGTACAAAGCTCGAGTGCCCTGGAAAAATGATGATAGGAGTGAG	1560
447	I E S S A O Y K A R V A L E N D D R S E	466
1561	GAAGAAAAATACACAGCAGTTTCAGAGAAATTCAGTGAACTGAGGGGCACAGCATAAAC	1620
467	E E K Y T A V O R N S S E R E G H S I N	486
1621	ACTAGGGAAAAATAAATATATTCTCTGGACAAAGAAATAGAGAAGTCATATCTTGGGGA	1680
487	T R E N K Y I P P G O R N R E V I S W G	506
1681	AGTGGGAGACAGAATTCACCGCGTATGGGCCAGCCTGGATCGGGCTCCATGCCATCAAGA	1740
507	S G R O N S P R M G O P G S G S M P S R	526
1741	TCCACTTCTCACACTTCAGATTTCAAACCCGAATTCCTGGTTCAGACCAAGAGTAGTTAAT	1800
527	S T S H T S D F N P N S G S D O R V V N	546
1801	GGAGGTGTTCCCTGGCCATCGCCTTGGCCATCTCCTTCCCTCGCCACCTTCTCGCTAC	1860
547	G G V P W F S P C P S P S S R P P S R Y	566
1861	CAGTCAGGTCCCAAGTCTCTTCACCTCGGGCAGCCACCCCTACACGGCCGCCCTCCAGG	1920
567	O S G P N S L P P R A A T P T R P P S R	586
1921	CCCCCTCGGGCCATCCAGACCCCCGTCTCACCCCTCTGCTCATGGTTCTCCAGCTCCT	1980
587	P P S R P P P S H F S A H G S P A P	606
1981	GTCTCTACTATGCCATAACGCATGTCTTCAGAAGGGCTCCAAGGATGTCCCCAAAGGCC	2040
607	V S T M F F R H S S E G P P R M S P K A	626
2041	CAGCGACATCCTCGAAATCACAGAGTTTCTGCTGGGAGGGGTTCATATCCAGTGGCCTA	2100
627	O R H P R H H R V S A G R G S I S S G L	646
2101	GAATTTGTATCCCAACCCACCCAGTGAGCAGCTACTCCTCCAGTAGCAAGGACCAGT	2160
647	E F V S H H P P S E A A T P P V A R T S	666
2161	CCCTCGGGGGGAACGTGGTCATCAGTGGTTCAGTGGGTTCCAAGATTATCCCTAAAACT	2220
667	P S G G T W S S V V S G V P R L S P K T	686
2221	CATAGACCCAGGTCTCCAGACAGAACAGTATTGGAAATACCCCAAGTGGGCCAGTTCTT	2280
687	H R P R S P R O N S I G N T P S G P V L	706
2281	GCTTCTCCCCAAGCTGGTATTATTCCAACCTGAAGCTGTTGCCATGCCATTTCAGCTGCA	2340
707	A S P O A G I I P T E A V A M P I P A A	726
2341	TCTCCTACGCCTGCTAGTCTGTCATCGAACAGAGCTGTTACCCCTTCTAGTGAGGCTAAA	2400
727	S P T P A S P A S H R A V T P S S E A K	746
2401	GATTCAGGCTTCAAGATCAGAGGCAGAACTCTCCTGCAGGGAATAAAGAAATATTTAAA	2460
747	D S R L O D O R O N S P A G N K E N I K	766
2461	CCCAATGAACATCAGCTAGCTTCTCAAAAGCTGAAAAACAAAGGTATATCACCAGTTGTT	2520
767	P N E T S P S F S K A E N K G I S P V V	786
2521	TCTGAACATAGAAAACAGATTGATGATTTAAAGAAATTTAAGAAATGATTTTAGGTTACAG	2580
787	S E H R K O I D D L K K F K N D F R L Q	806
2581	CCAAGTTCTACTTCTGAATCTATGGATCAACTACTAAACAAAAATAGAGAGGGAGAAAAA	2640
807	P S S T S E S M D O L L N K N R E G E K	826
2641	TCAAGAGATTGTATCAAGACAAAAATTGAACCAAGTGCTAAGGATTCTTTTATTGAAAT	2700
827	S R D L I K D K I E P S A K D S F I E N	846
2701	AGCAGCAGCAACTGTACCAAGTGGCAGCAGCAAGCCGAATAGCCCCAGCATTTCCCCCTCA	2760
847	S S S H C T S G S S K P N S P S I S P S	866
2761	ATACTTAGTAACACGGAGCACAAGAGGGGACCTGAGGTCACTTCCCAAGGGGTTTCAGACT	2820
867	I L S N T E H K R G P E V T S Q G V Q T	886
2821	TCCAGCCAGCATGTAAACAAAGAGAAAGACGATAAGGAAGAGAAGAAAGACCGAGCTGAG	2880
887	S S P A C F O E K D D K E E K K D A A E	906
2881	CAAGTTAGGAATCAAAATTGAATCCCAATGCAAGGAGTTCAACCCACGTTCTTCTCT	2940
907	O V R K S T L H P N A K E F N P R S F S	926
2941	CAGCCAAAGCCTTCTACTAGCCCAACTTCACCTCGGCCTCAAGCACAACTAGCCCATCT	3000
927	O P K P S T I P T S P R P O A O P S P S	946
3001	ATGGTGGGTGATCAACAGCCAACTCCAGTTTATACTCAGCCTGTTTGTITGCACCAAT	3060
947	H V G H O O P T P V Y T O P V C F A P N	966
3061	ATGATGTATCCAGTCCCAAGTGAAGCCAGGCGTGCAACCTTTATACCAATACCTATGACG	3120
967	M M Y P V P V S P G V O P L Y P I P M T	986

FIGURE 6B

86T50" 866T8680

3121	CCCATGCCAGTGAATCAAGCCAAAGACATATAGAGCAGTACCAAATATGCCCCAAACAGCGG	3180
987	P M P V N O A K T Y R A V P N M P O O R	1006
3181	CAAGACCAGCATCATCAGAGTGCCATGATGCCACCCAGCGTCAGCAGCGGGCCCCACCGATT	3240
1007	O D Q H H O S A M H H P A S A A G P P I	1026
3241	GCAGCCACCCACAGGTTACTCCACGCAATATGTTGCCCTACAGTCTCTCAGCAGTTCCTCA	3300
1027	A A T P P A Y S T O Y V A Y S P O O F P	1046
3301	AATCAGCCCCCTTGTTCAGCATGTGCCACATTATCAGTCTCAGCATCTCTCATGTCTATAGT	3360
1047	N O P L V O H V P H Y O S O H P H V Y S	1066
3361	CCTGTAATACAGGGTAATGCTAGAATGATGGCACCAACACACGCCCAGCCTGGTTTA	3420
1067	P V I O G N A R M M A P P T H A O P G L	1086
3421	GTATCTTCTTTCAGCAACTCAGTACGGGGCTCATGAGCAGACGCGATGCGATGTATGCATGT	3480
1087	V S S S A T O Y G A H E O T H A M Y A C	1106
3481	CCCAAATTACCATACAAACAGGAGACAAGCCCTTCTTCTACTTTTGCCATTTCCACGGGC	3540
1107	P K L P Y N K E T S P S F Y F A I S T G	1126
3541	TCCCTTGCTCAGCAGTATGGCACCCCTAACGCTACCCCTGCACCCACATACTCCACACCCCT	3600
1127	S L A O O Y A H P N A T L H P H T P H P	1146
3601	CAGCCTTCAGCTACCCCACTGGACAGCAGCAAGCCAAACATGGTGGAAGTCATCCTGCA	3660
1147	Q P S A T P T G O O Q S O H G G S H P A	1166
3661	CCCAGTCCTGTTTCAGCAGCATCAGCACCCAGGCCCGCCAGGCTCTCCATCTGGCCAGTCCA	3720
1167	P S P V O H H O H O A A O A L H L A S P	1186
3721	CAGCAGCAGTCAGGCATTTACCACGGGGGGCTTGCGCCAACTCCACCCCTCCATGACACCT	3780
1187	Q O O S A I Y H A G L A P T P P S M T P	1206
3781	GCCTCCAAACAGCAGTCGCCACAGAATAGTTTTCCACAGCAGCACAAACAGACTGTCTTTACG	3840
1207	A S N T O S P O H S F P A A O Q T V F T	1226
3841	ATCCATCCTTCTCACTTTCAGCCGGCGTATACCAACCCACCCCAATGGCCCCACGTACCT	3900
1227	I H P S H V O P A Y T N P P H M A H V P	1246
3901	CAGGCTCATGTACAGTCAGGAATGGTTCTTCTCATCCAACCTGCCCATGCGCCAATGATG	3960
1247	Q A H V O S G M V P S H P T A H A P M M	1266
3961	CTAATGACGACACAGCCACCCGGCGGTCCCCAGGCCGCCCTCGCTCAAGTGCACTACAG	4020
1267	L M T T O P P G G P Q A A L A Q S A L Q	1286
4021	CCCATTCAGTCTCGACAAACAGCGCATTTCCCTTATATGACGCACCCCTTCAGTACAAGCC	4080
1287	P I P V S T T A H F P Y M T H P S V Q A	1306
4081	CACCACCAACAGCAGTTGTAAAGGCTGCCCTGGAGGAACCGAAAGGCCAAATTCCCTCCTC	4140
1307	H H O O O L	1326
4141	CCTTCTACTGCTTCTACCAACTGGAAGCACAGAAAAGTGAATTTCAITTTATTTTGTITTT	4200
4201	TAAATATATATGTTGATTTCTTGTAAACATCCAATAGGAATGCTAACAGTTCACTTGCAAG	4260
4261	TGGAAGATACTTGGACCGAGTAGAGGCATTTAGGAAGTTGGGGGCTATTCCATAATTCCA	4320
4321	TATGCTGTTTTCAGAGTCCCGCAGGTACCCACAGCTCTGCTTGCCGAAACTGGAAGTTAATT	4380
4381	ATTTTITTAATAACCCCTTGAAGTTCATGAACACATCAGCTAGCAAAAGAAGTAAACAAAGAGT	4440
4441	GATTCCTTGCTGCTATTACTGCTAAAAAAAAAAAAAAAAAAAAA 4481	

FIGURE 6C

	1		50
Ataxin-2	VYGFPLTMSLK	PQ000000000	0000000000
Mouse Ataxin-2	HEGFPLTMSLK	PQIPQ.....PPAPAT
A2RPLA	POPPPPOOHQ	ER.....
ConsensusL-	PQ.....
	51		100
Ataxin-2	ASFAAAPSPS	SSSVSSSSAT	APSSVVA...
Mouse Ataxin-2	SSPGAAPAS	AAVTSASVVP	APAAPVASSS
A2RP	..PGAAAIGS	A.....RGQSTGKGP
Consensus	..P-AA---S-RG---KG-
	101		150
Ataxin-2	POSTISFDGI	YANMRMVHIL	TSVVGSKCEV
Mouse Ataxin-2	PORTISFDGI	YANVRMVHIL	TSVVGSKCEV
A2RP	POSPI.FEGV	YHNSRMLHFL	TAVVGSTCDV
Consensus	PQ----F-G-	Y-H-RM-H-L	T-VVGS-C-V
	151		200
Ataxin-2	LVLDAANHEKS	TESSSGPKRE	EIMESILFKC
Mouse Ataxin-2	LVLDAANHEKS	TESSSGPKRE	EIMESVLFKC
A2RP	LAVDAVHRKA	SEPAGGPRRE	DIVDTMVFKP
Consensus	L--DA-H-K-	-E---GP-RE	-I-----FK-
	201		250
Ataxin-2	FTDSAIS..A	KVNGEHKEKD	LEPWDAGELT
Mouse Ataxin-2	FTDSALS..A	KVNGEHKEKD	LEPWDAGELT
A2RP	FTDSAIAMNS	KVNGEHKEKV	LQRWEGGD.S
Consensus	FTDSA-----	KVNGEHKEK-	L--W--G---
	251		300
Ataxin-2	MERYNEENYG	VVSTYDSSL	SYTVPLERDN
Mouse Ataxin-2	MERYNEENYG	VVSTYDSSL	SYTVPLERDN
A2RP	MFKFNEENYG	VKTTYDSSL	SYTVPLEKDN
Consensus	MF--NEENYG	V--TYDSSL	SYTVPLE-DN
	301		350
Ataxin-2	SAQYKARVAI	ENDD.RSEEE	KYTAVQRNCS
Mouse Ataxin-2	SAQYKARVAI	ENDD.RSEEE	KYTAVQRNCS
A2RP	SPOYRLRIAM	ENDDGRTEEE	KHSVQRQGS
Consensus	S-QY--R-A-	ENDD-R-EEE	K--AVQR--S
	351		
Ataxin-2	NR		
Mouse Ataxin-2	NR		
A2RP	..		
Consensus	--		

FIGURE 7

SCA2 Gene

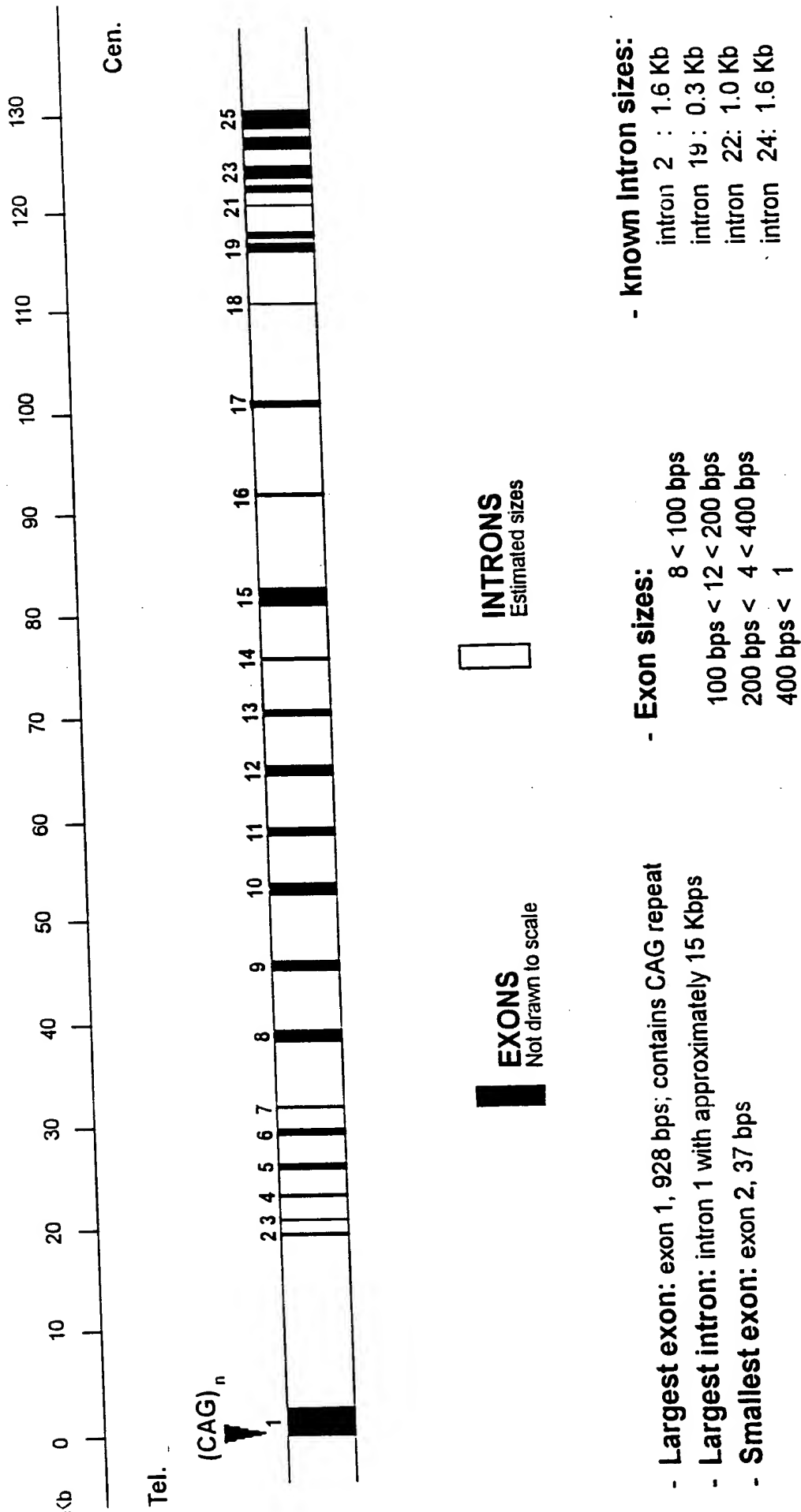


FIGURE 8